

endo sequence from Collagen XVIII.

Sequence Range: 1-555

Nucleotide 1 = Start for Endostatin and fragments EM1 and EM2.

EM1 fragment ends at nucleotide 525, EM2 fragment ends at nucleotide 501.

	5	10	15	20	25	30	35	40	45							
	CAT	ACT	CAT	CAG	GAC	TTT	CAG	CCA	GTG	CTC	CAC	CTG	GTG	GCA	CTG	AAC
	GTA	TGA	GTA	GTC	CTG	AAA	GTC	GGT	CAC	GAG	GTG	GAC	CAC	CGT	GAC	TTG
50		55	60		65	70	75		80	85	90		95			
	ACC	CCC	CTG	TCT	GGA	GGC	ATG	CGT	GGT	ATC	CGT	GGA	GCA	GAT	TTC	CAG
	TGG	GGG	GAC	AGA	CCT	CCG	TAC	GCA	CCA	TAG	GCA	CCT	CGT	CTA	AAG	GTC
100		105		110		115	120		125		130	135		140		
	TGC	TTC	CAG	CAA	GCC	CGA	GCC	GTG	GGG	CTG	TCG	GGC	ACC	TTC	CGG	GCT
	ACG	AAG	GTC	GTT	CGG	GCT	CGG	CAC	CCC	GAC	AGC	CCG	TGG	AAG	GCC	CGA
145		150		155		160	165		170		175	180		185	190	
	TTC	CTG	TCC	TCT	AGG	CTG	CAG	GAT	CTC	TAT	AGC	ATC	GTG	CGC	CGT	GCT
	AAG	GAC	AGG	AGA	TCC	GAC	GTC	CTA	GAG	ATA	TCG	TAG	CAC	GCG	GCA	CGA
195		200		205		210	215		220		225	230		235	240	
	GAC	CGG	GGG	TCT	GTG	CCC	ATC	GTC	AAC	CTG	AAG	GAC	GAG	GTG	CTA	TCT
	CTG	GCC	CCC	AGA	CAC	GGG	TAG	CAG	TTG	GAC	TTC	CTG	CTC	CAC	GAT	AGA
245		250		255		260	265		270		275	280		285		
	CCC	AGC	TGG	GAC	TCC	CTG	TTT	TCT	GGC	TCC	CAG	GGT	CAA	CTG	CAA	CCC
	GGG	TCG	ACC	CTG	AGG	GAC	AAA	AGA	CCG	AGG	GTC	CCA	GTT	GAC	GTT	GGG
290		295		300		305	310		315		320	325		330	335	
	GGG	GCC	CGC	ATC	TTT	TCT	TTT	GAC	GGC	AGA	GAT	GTC	CTG	AGA	CAC	CCA
	CCC	CGG	GCG	TAG	AAA	AGA	AAA	CTG	CCG	TCT	CTA	CAG	GAC	TCT	GTG	GGT
340		345		350		355	360		365		370	375		380		
	GCC	TGG	CCG	CAG	AAG	AGC	GTA	TGG	CAC	GGC	TCG	GAC	CCC	AGT	GGG	CGG
	CGG	ACC	GGC	GTC	TTC	TCG	CAT	ACC	GTG	CCG	AGC	CTG	GGG	TCA	CCC	GCC
385		390		395		400	405		410		415	420		425	430	
	AGG	CTG	ATG	GAG	AGT	TAC	TGT	GAG	ACA	TGG	CGA	ACT	GAA	ACT	ACT	GGG
	TCC	GAC	TAC	CTC	TCA	ATG	ACA	CTC	TGT	ACC	GCT	TGA	CTT	TGA	TGA	CCC
435		440		445		450	455		460		465	470		475	480	
	GCT	ACA	GGT	CAG	GCC	TCC	TCC	CTG	CTG	TCA	GGC	AGG	CTC	CTG	GAA	CAG
	CGA	TGT	CCA	GTC	CGG	AGG	AGG	GAC	GAC	AGT	CCG	TCC	GAG	GAC	CTT	GTC
485		490		495		500	505		510		515	520		525		
	AAA	GCT	GCG	AGC	TGC	CAC	AAC	AGC	TAC	ATC	GTC	CTG	TGC	ATT	GAG	AAT
	TTT	CGA	CGC	TCG	ACG	GTG	TTG	TCG	ATG	TAG	CAG	GAC	ACG	TAA	CTC	TTA
530		535		540		545	550		555							
	AGC	TTC	ATG	ACC	TCT	TTC	TCC	AAA	TAG							
	TCG	AAG	TAC	TGG	AGA	AAG	AGG	TTT	ATC							

Fig. 1

Sequence Range: 1 to 184

5	10	15	20	25	30	35	40	45						
HTH	QDF	QPV	LHL	VAL	NTP	LSG	GMR	GIR	GAD	FQC	FQQ	ARA	VGL	SGT
50	55	60	65	70	75	80	85	90						
FRA	FLS	SRL	QDL	YSI	VRR	ADR	GSV	PIV	NLK	DEV	LSP	SWD	SLF	SGS
95	100	105	110	115	120	125	130	135						
QGQ	LQP	GAR	IFS	FDG	RDV	LRH	PAW	PQK	SVW	HGS	DPS	GRR	LME	SYC
140	145	150	155	160	165	170	175	180						
ETW	RTE	TTG	ATG	QAS	SLL	SGR	LLE	QKA	ASC	HNS	YIV	LCI	ENS	FMT
SFS	K													

Fig. 2

FIG. 3

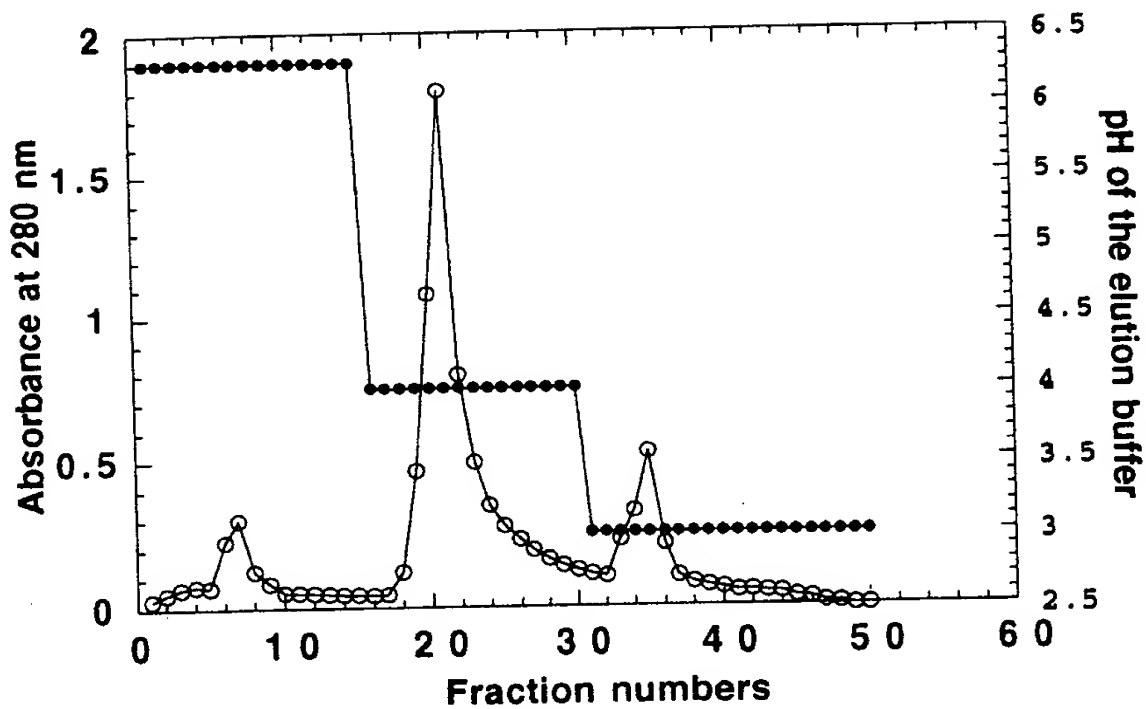


FIG. 4

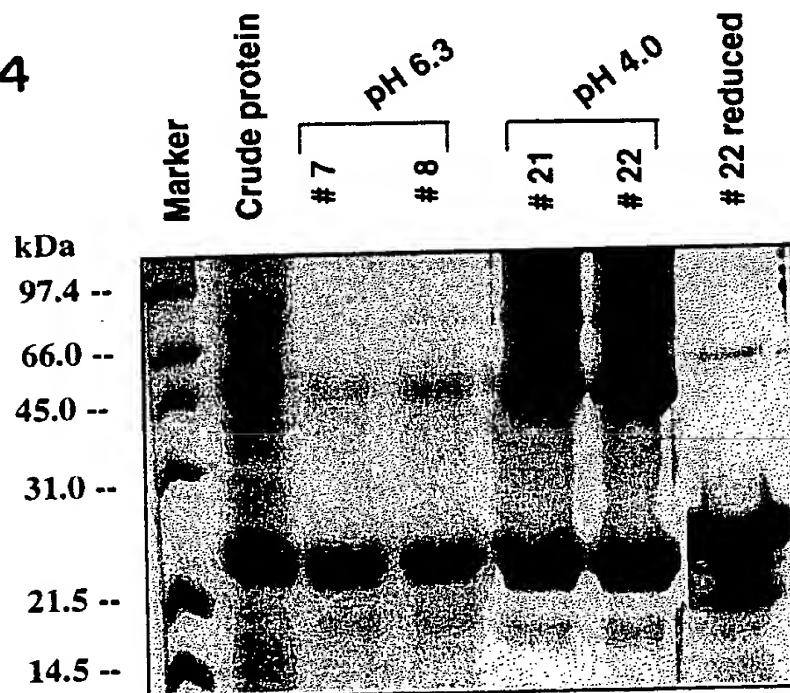


FIG.5

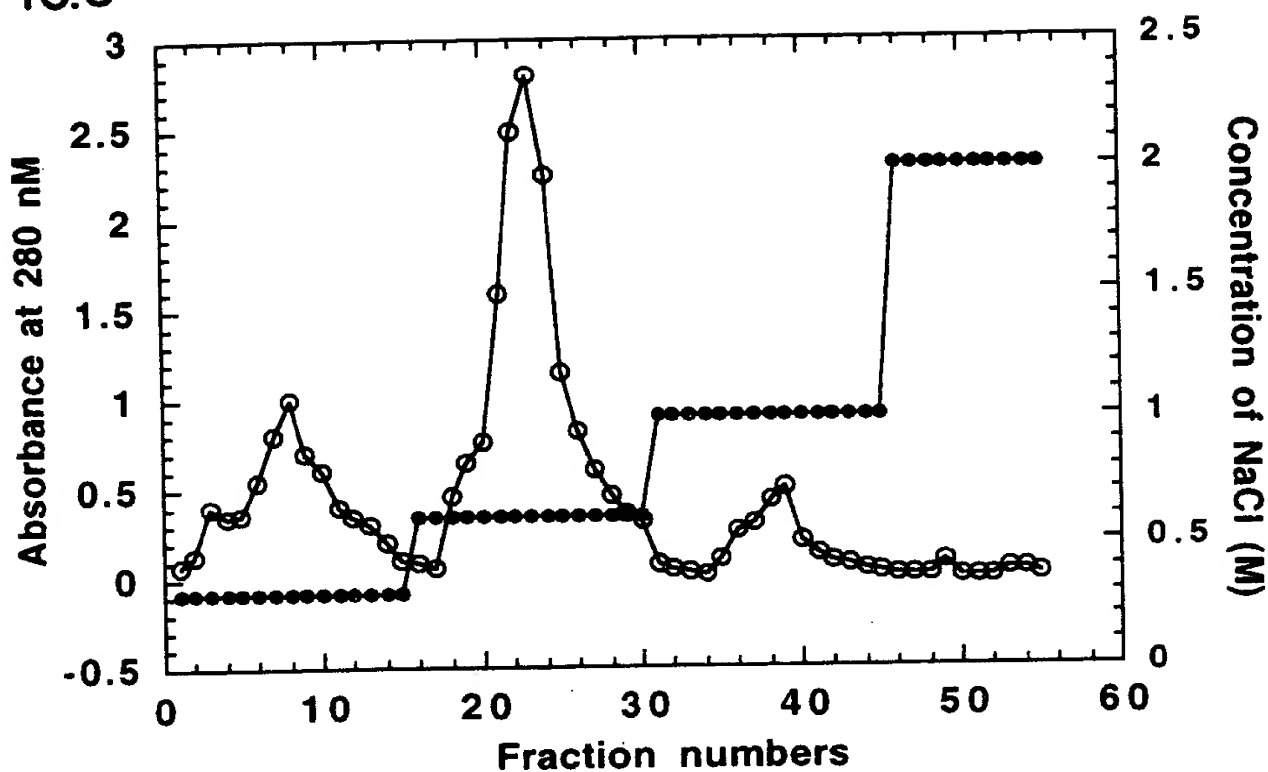


FIG.6

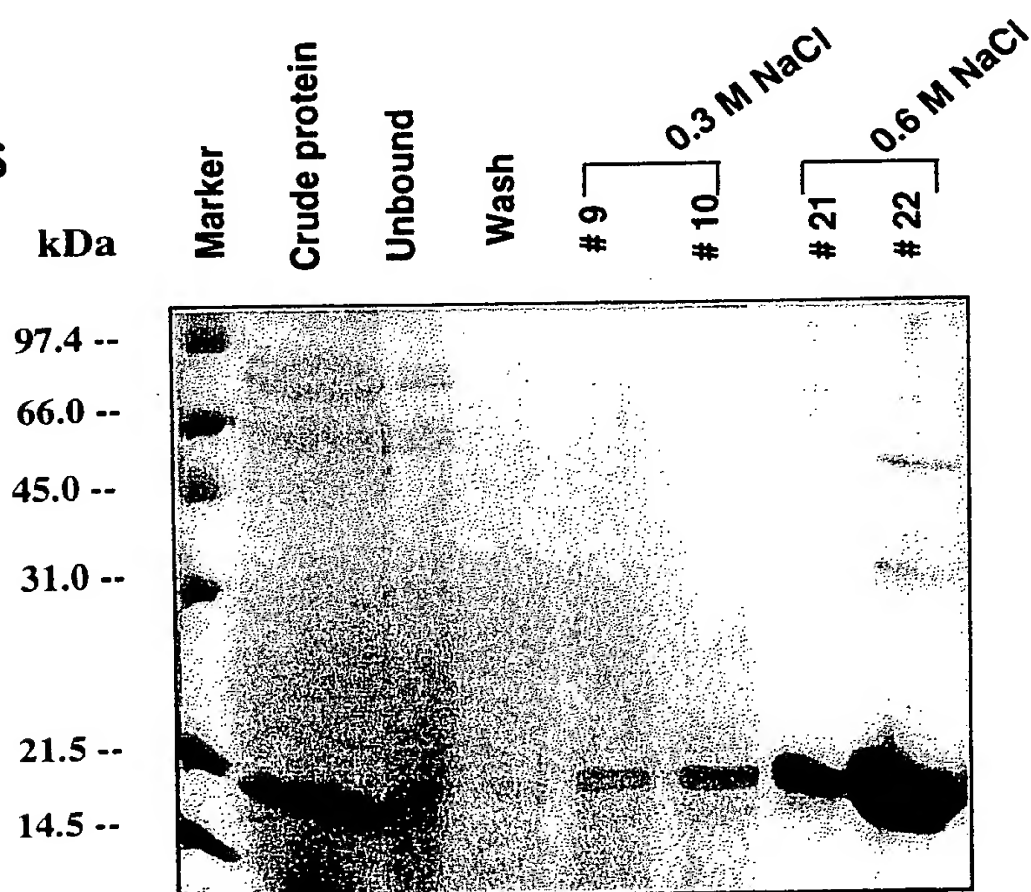


FIG. 7

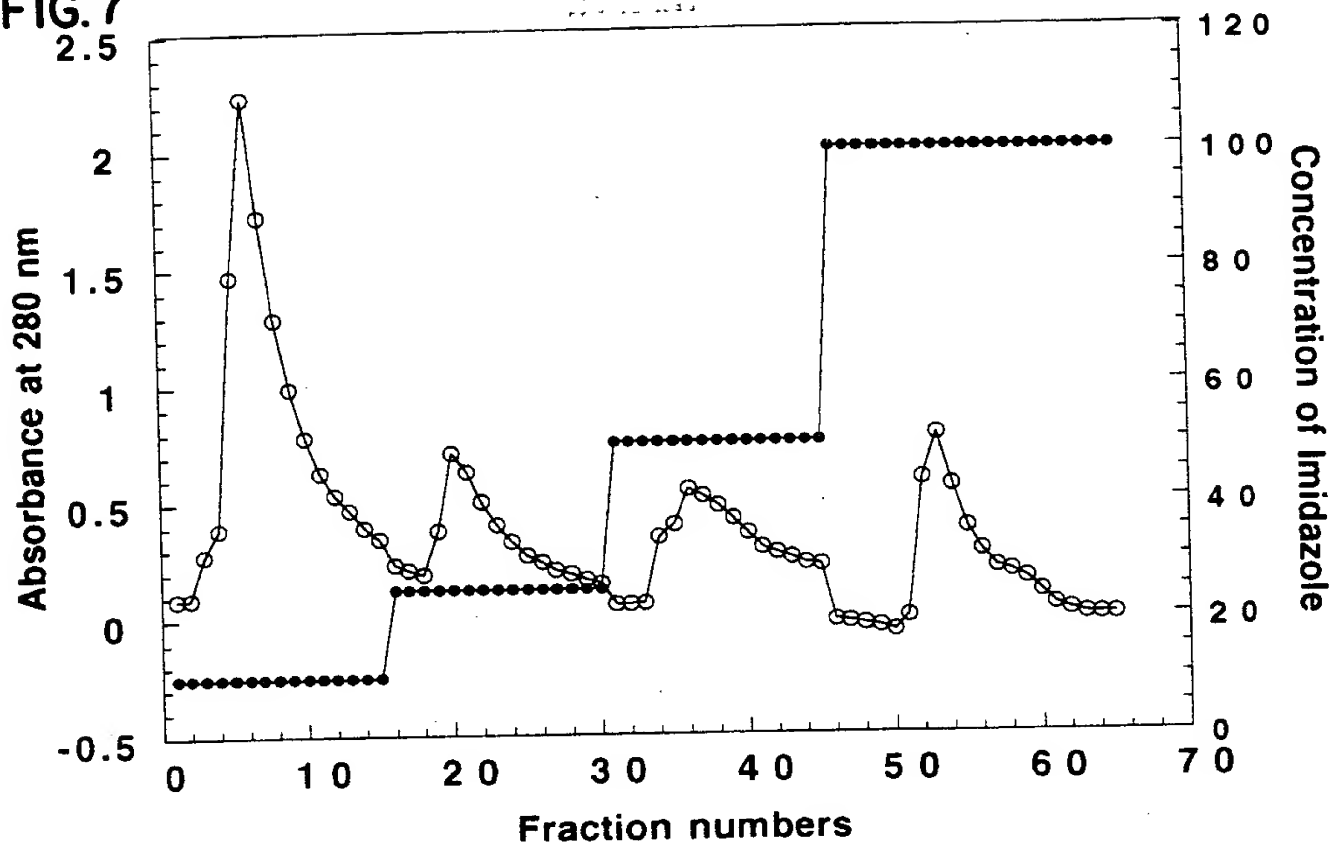
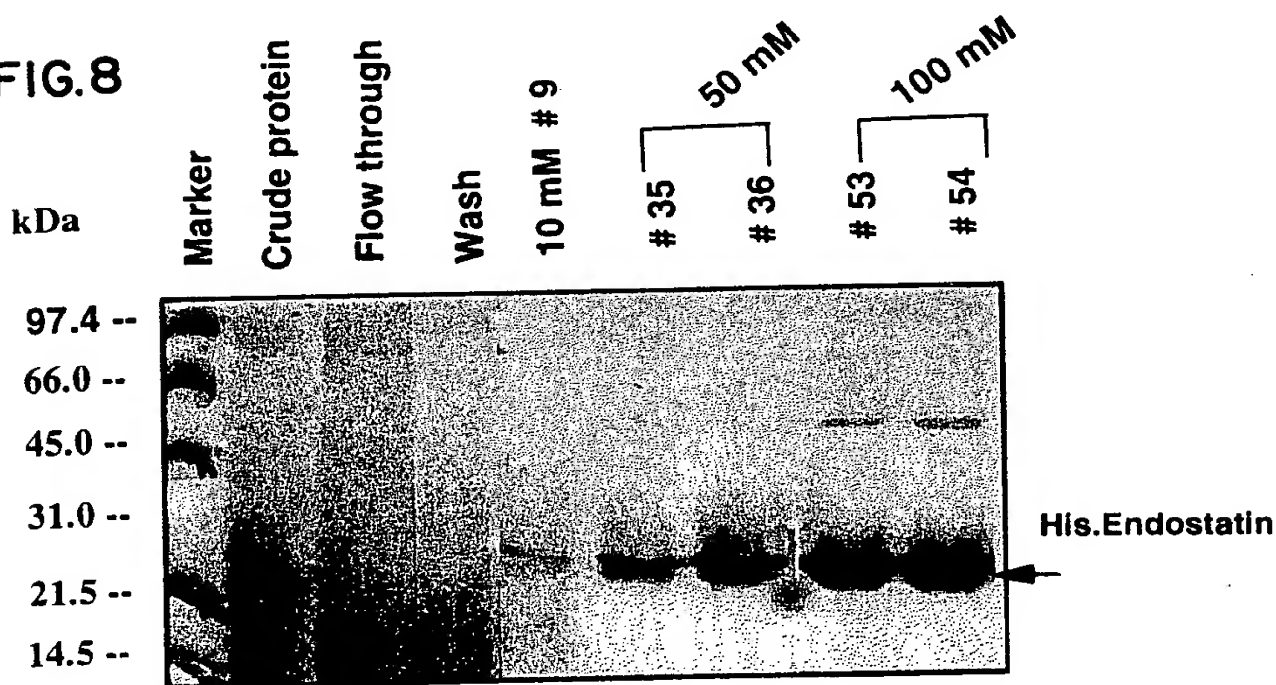


FIG. 8



His.endostatin (bacteria)  
Endostatin (Yeast)  
His.endostatin (yeast)

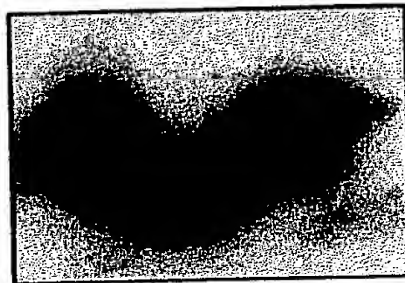
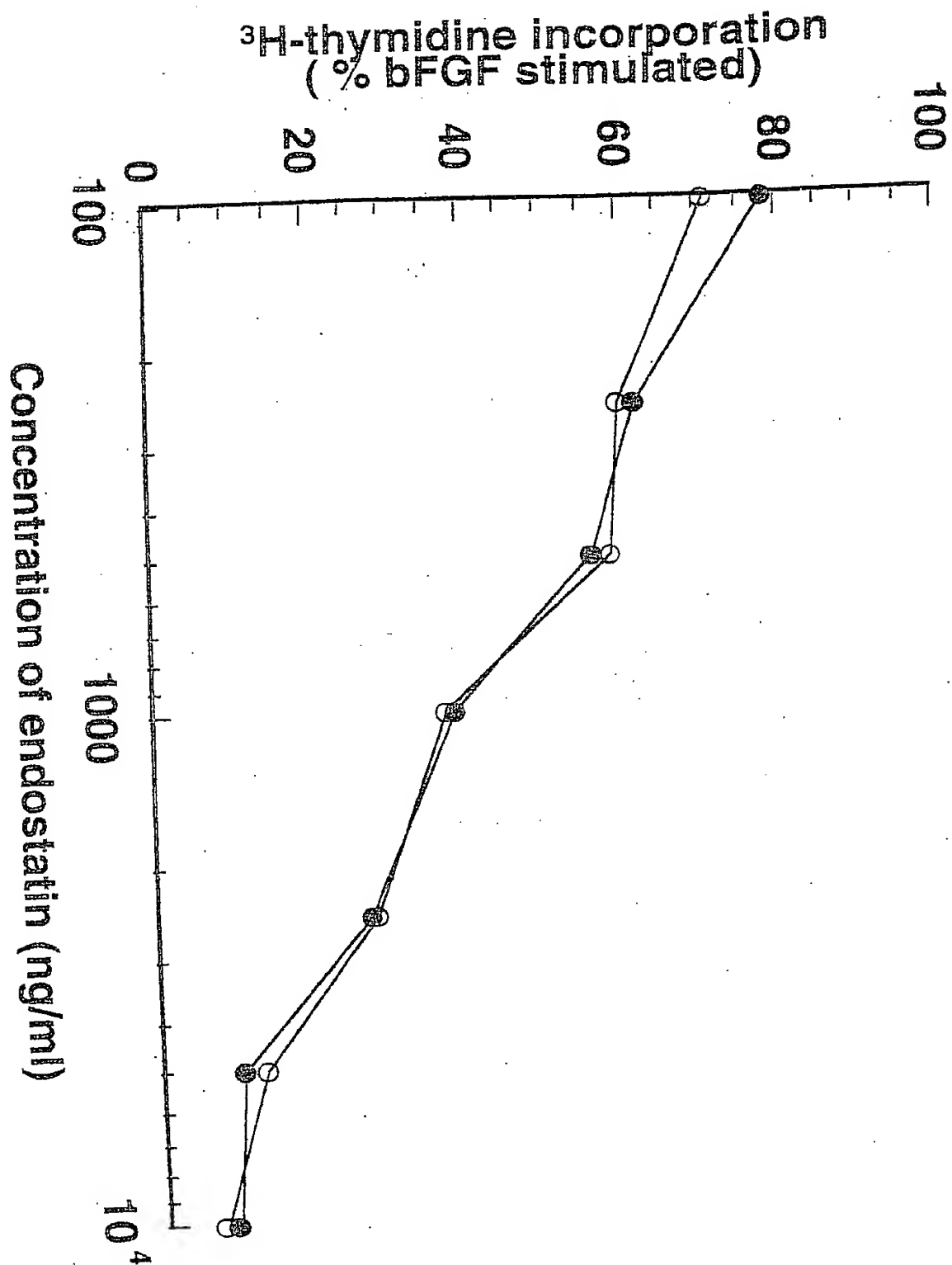


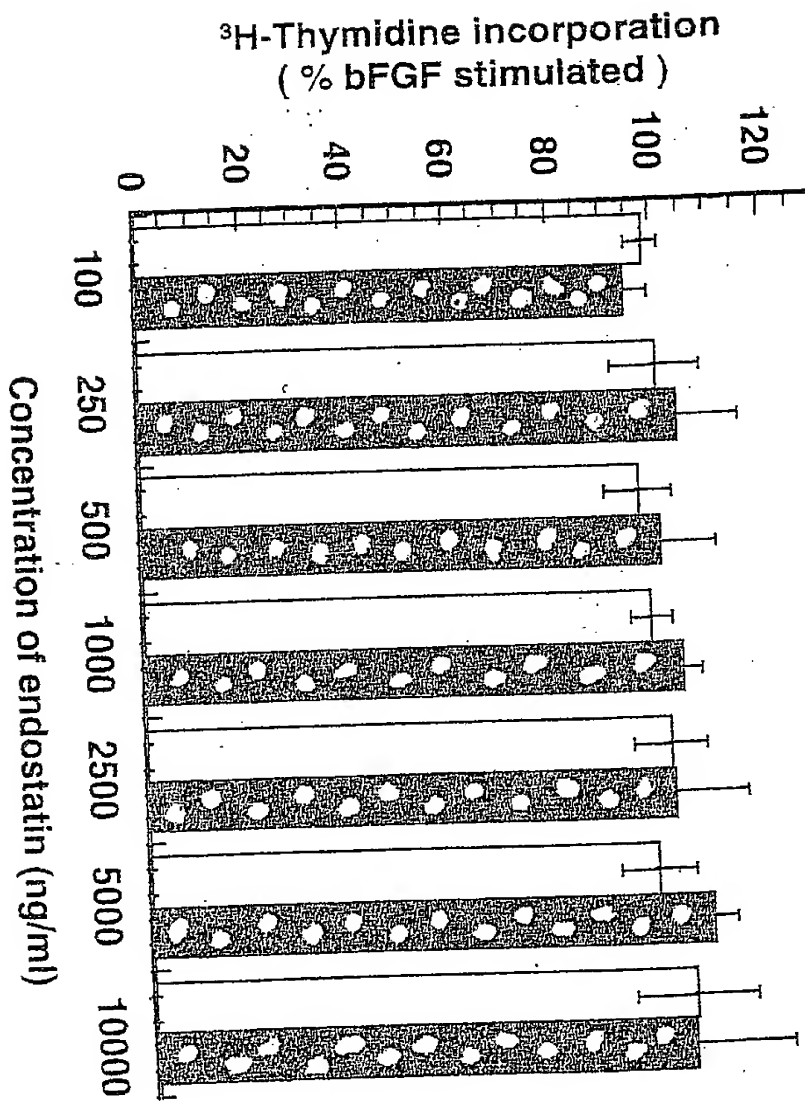
Fig. 10



0958977 000000

1440.1023-011

Fig. 11



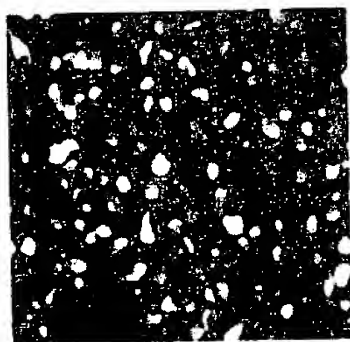
0058977-060800

Fig. 11

1440.1623-011

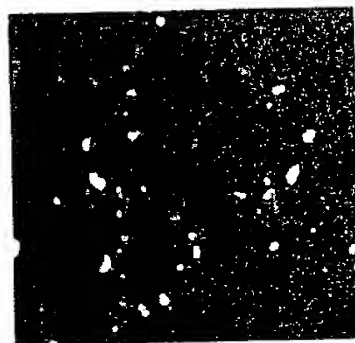


FIG. 12 A



Control +bFGF

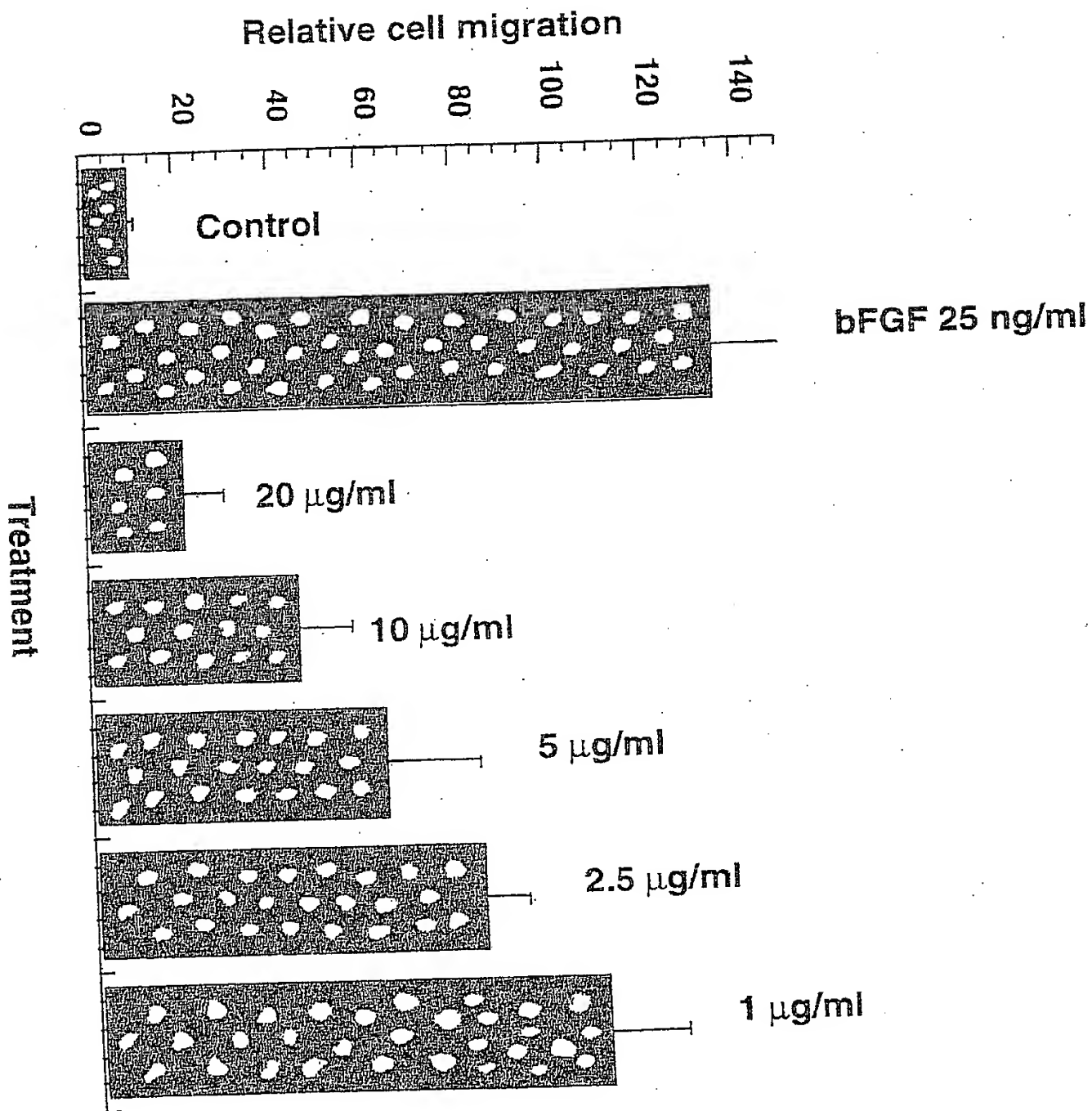
FIG. 12 B



Endostatin 20  $\mu$ g/ml

000000 7768560

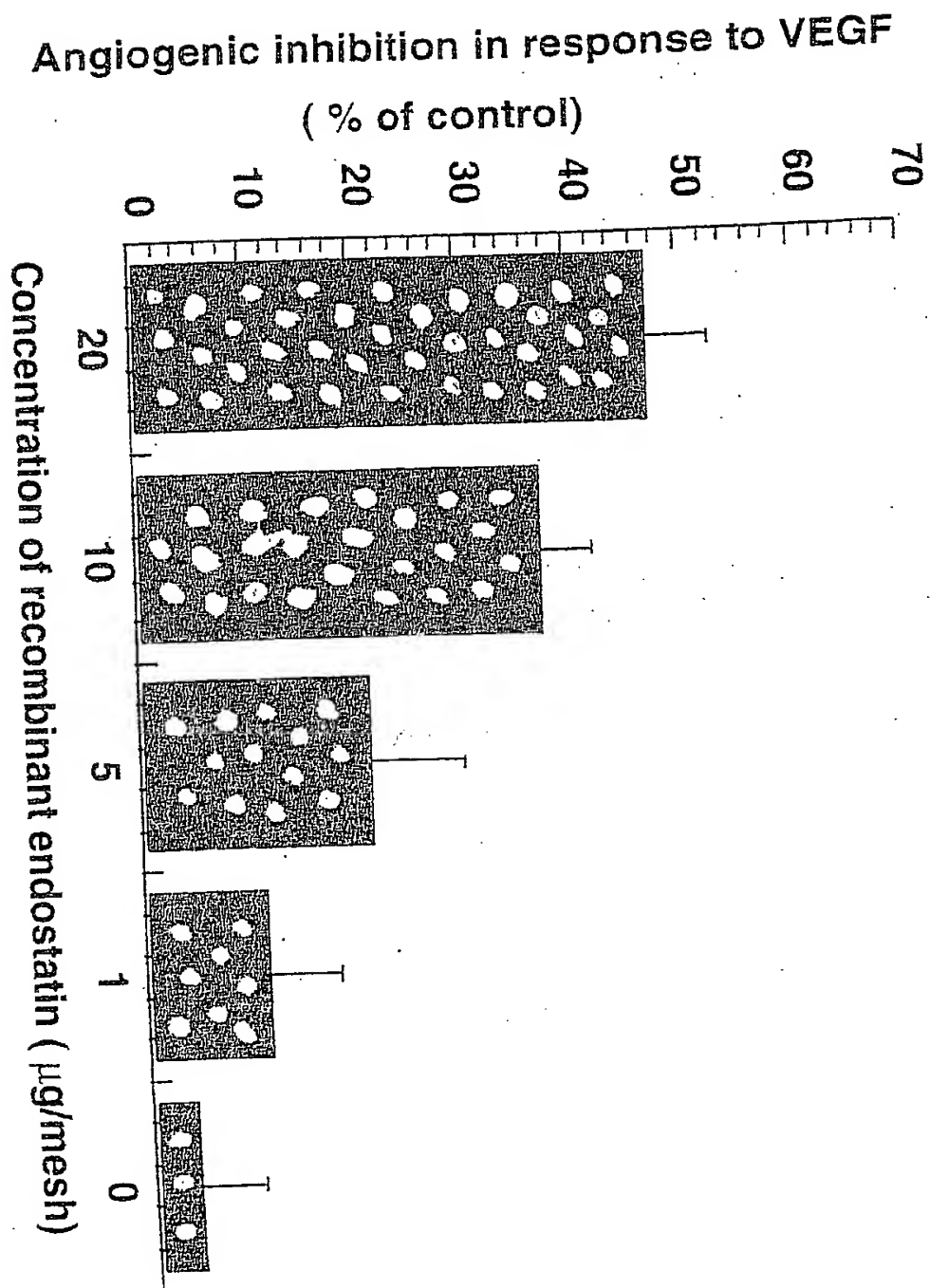
Fig. 13



00589777 060800

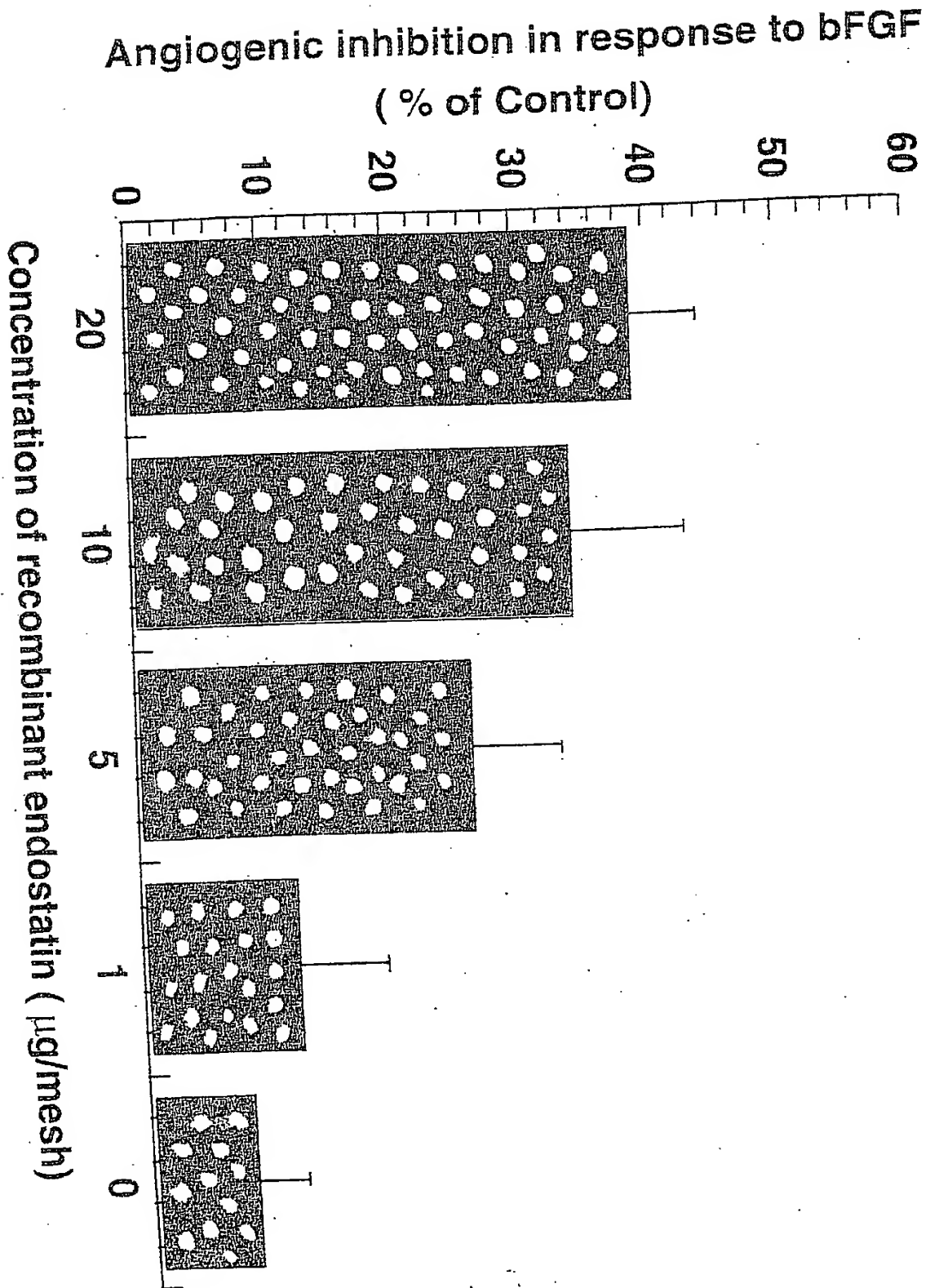
**VEGF +  
endostatin 20  $\mu$ g**

Fig. 15A



0058077 060900

Fig. 15B



00580777 00508000

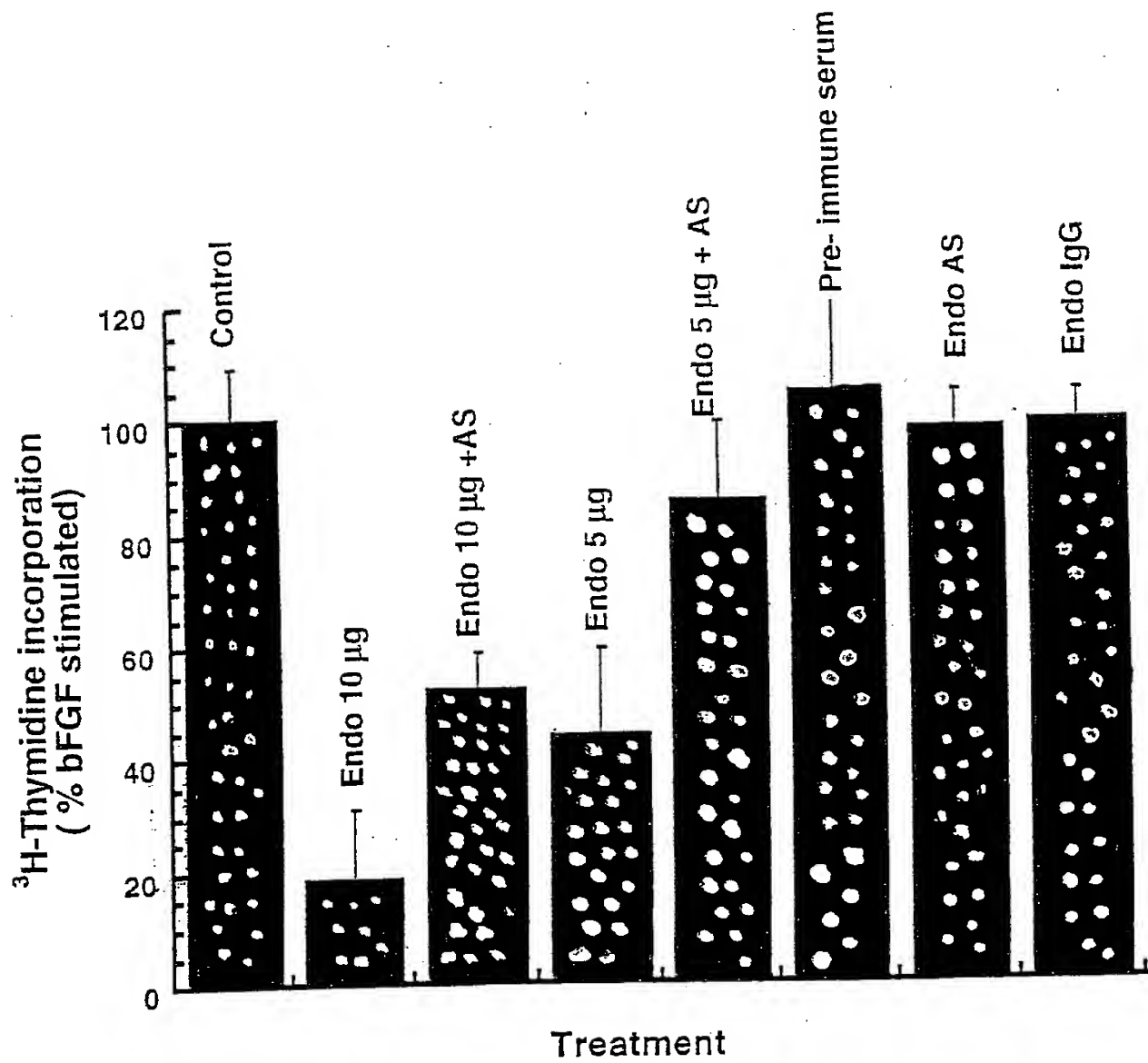
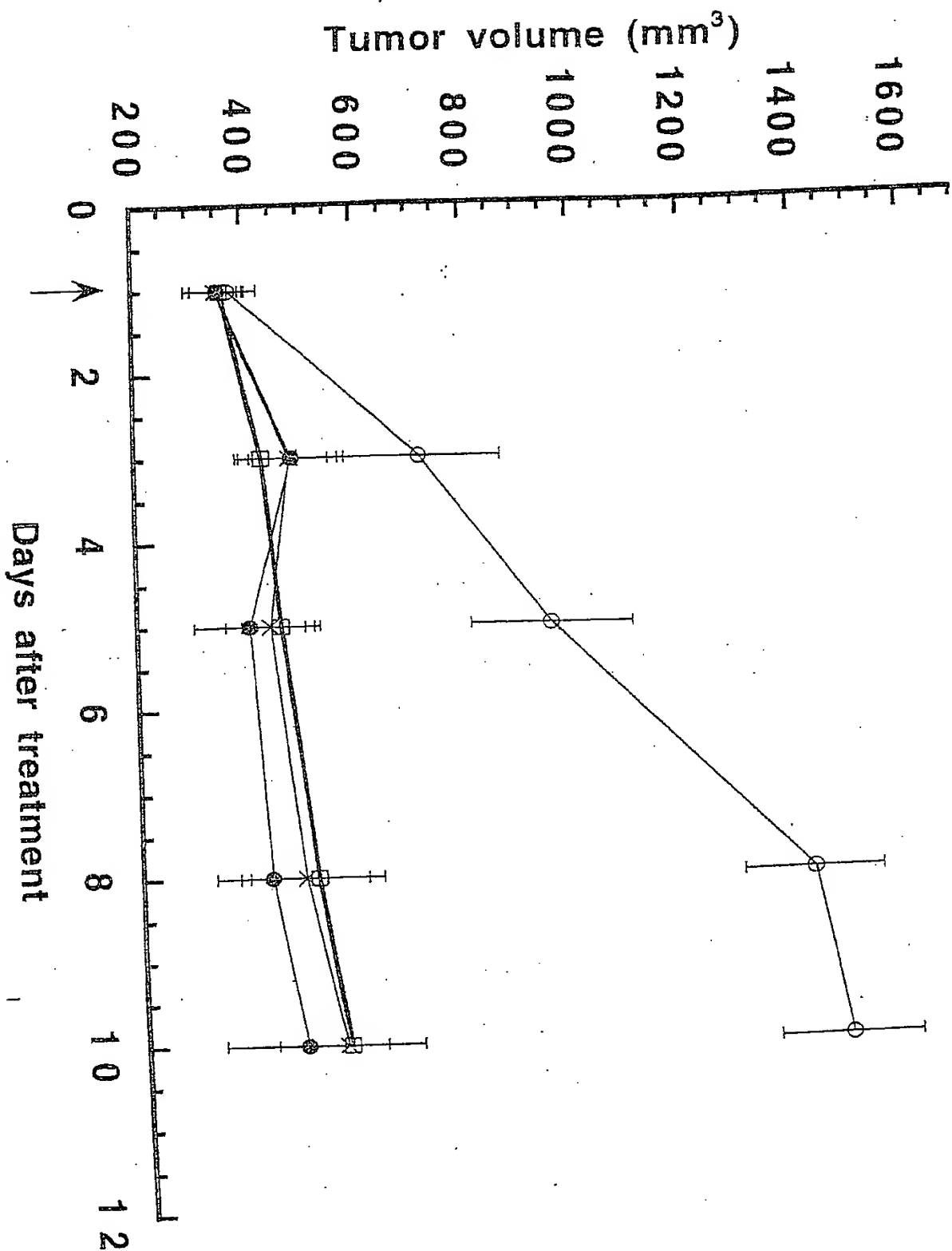


Fig. 16

**VEGF + endostatin (10 µg) +  
polyclonal antiserum (50 µg)**

Fig. 18

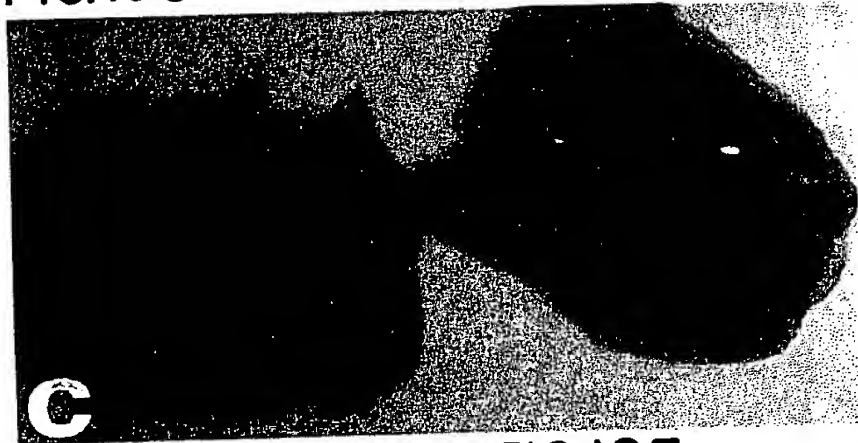
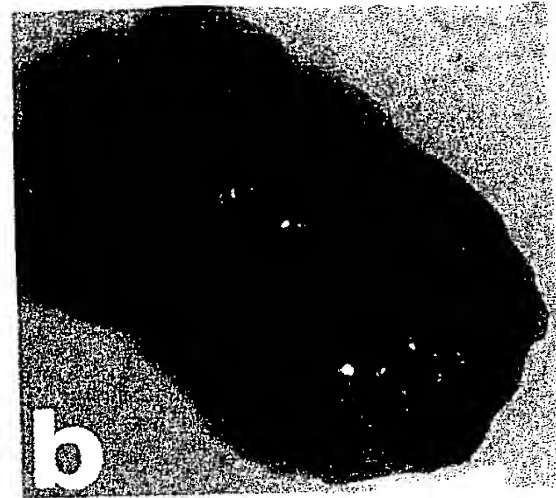


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**FIG. 19E**

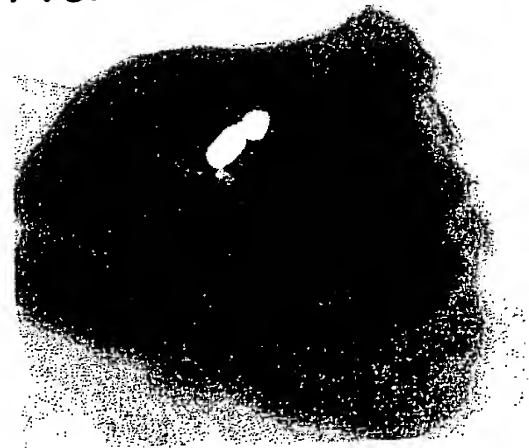
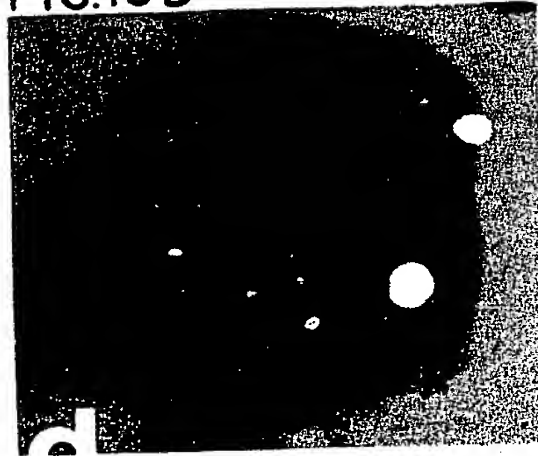
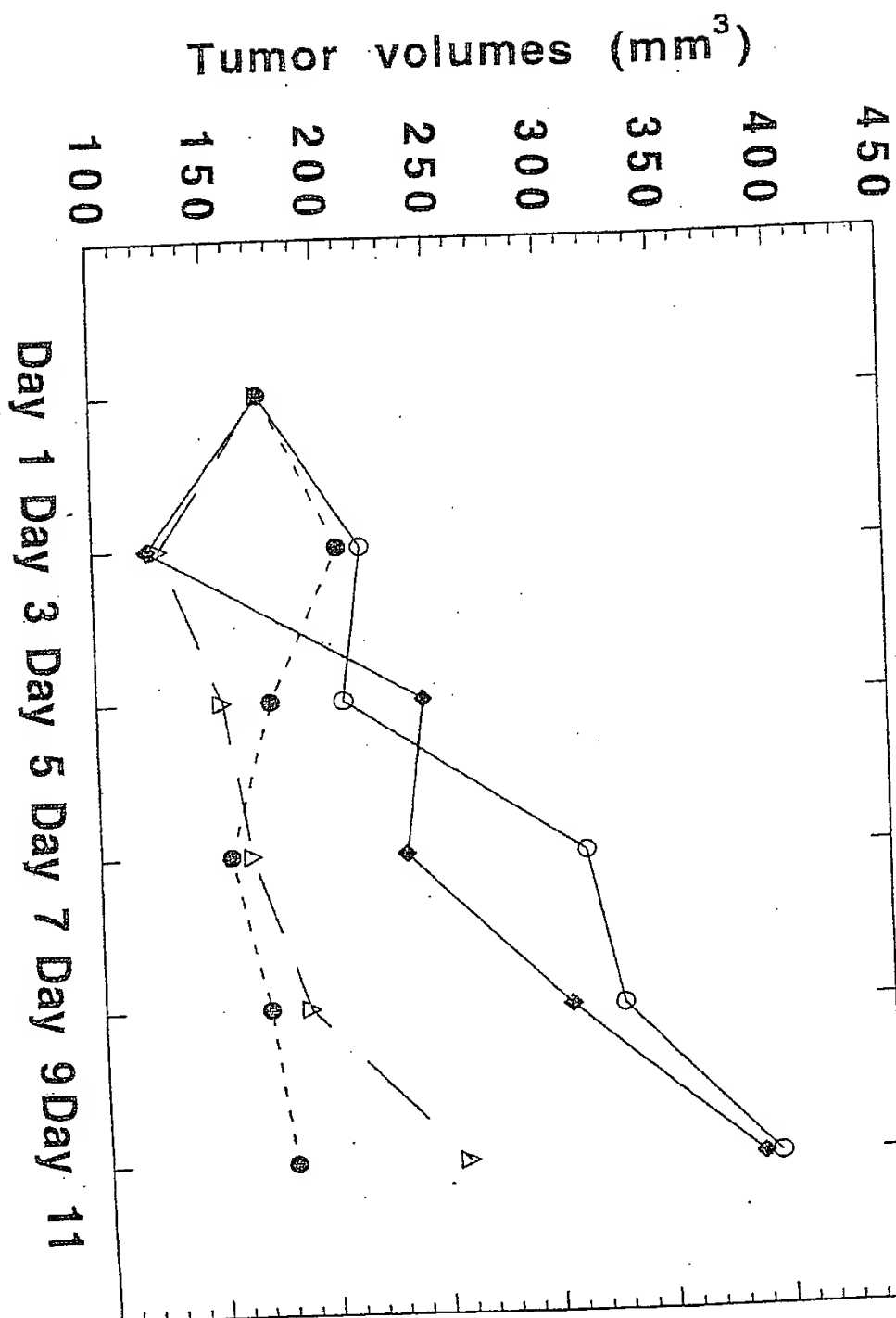


Fig. 20



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Fig. 21

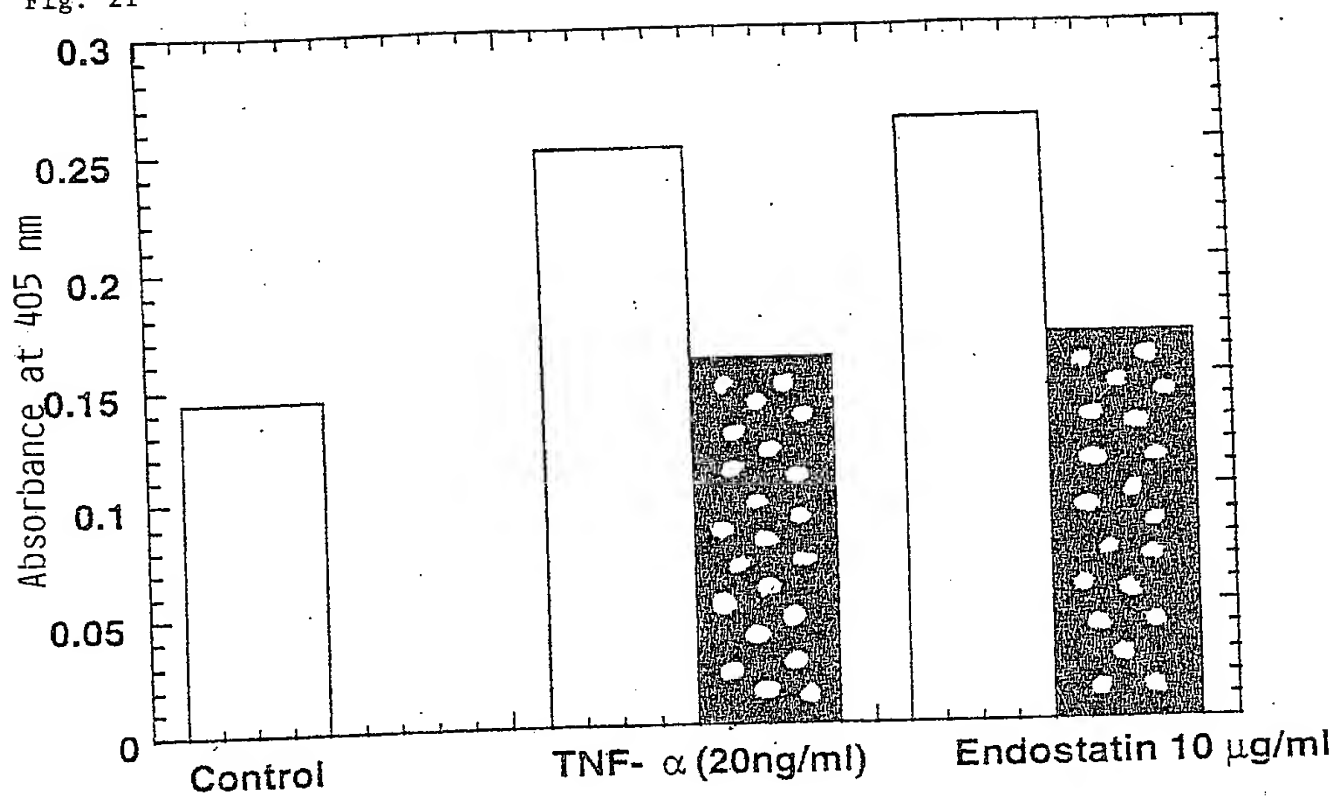


Fig. 22

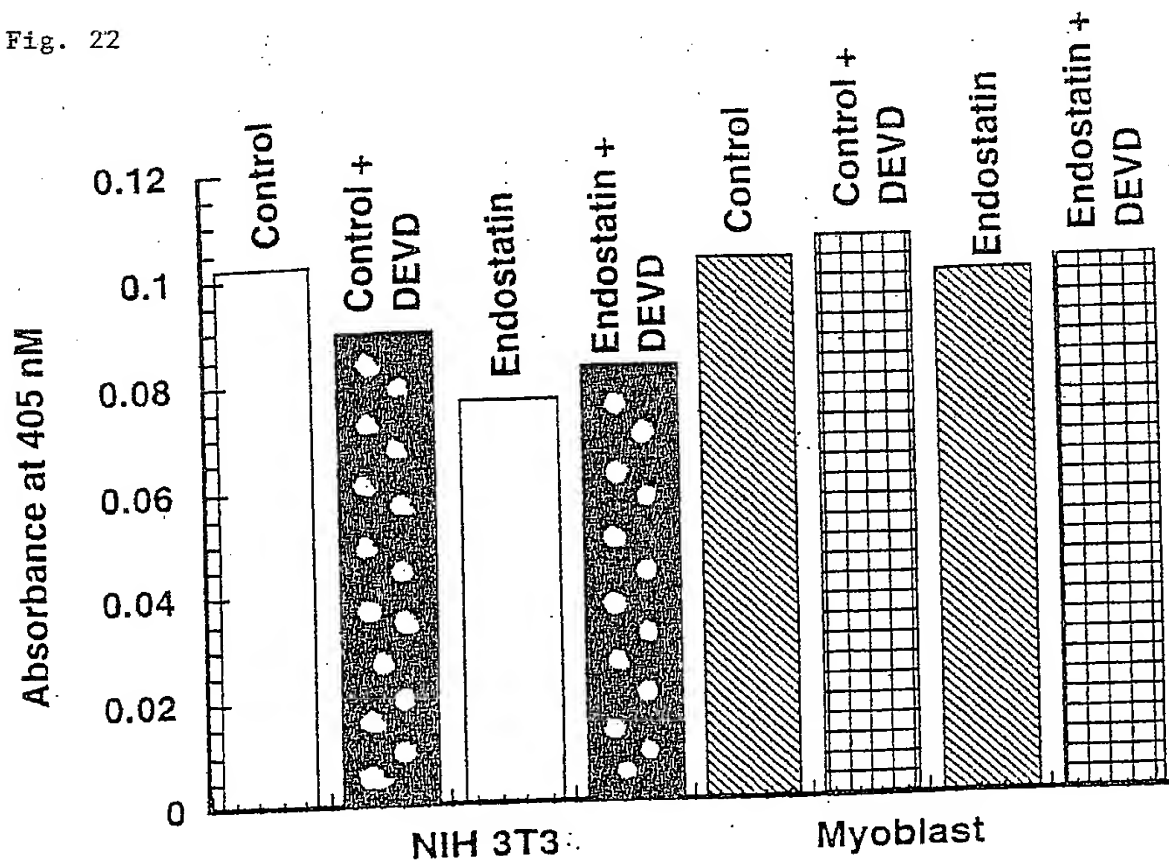
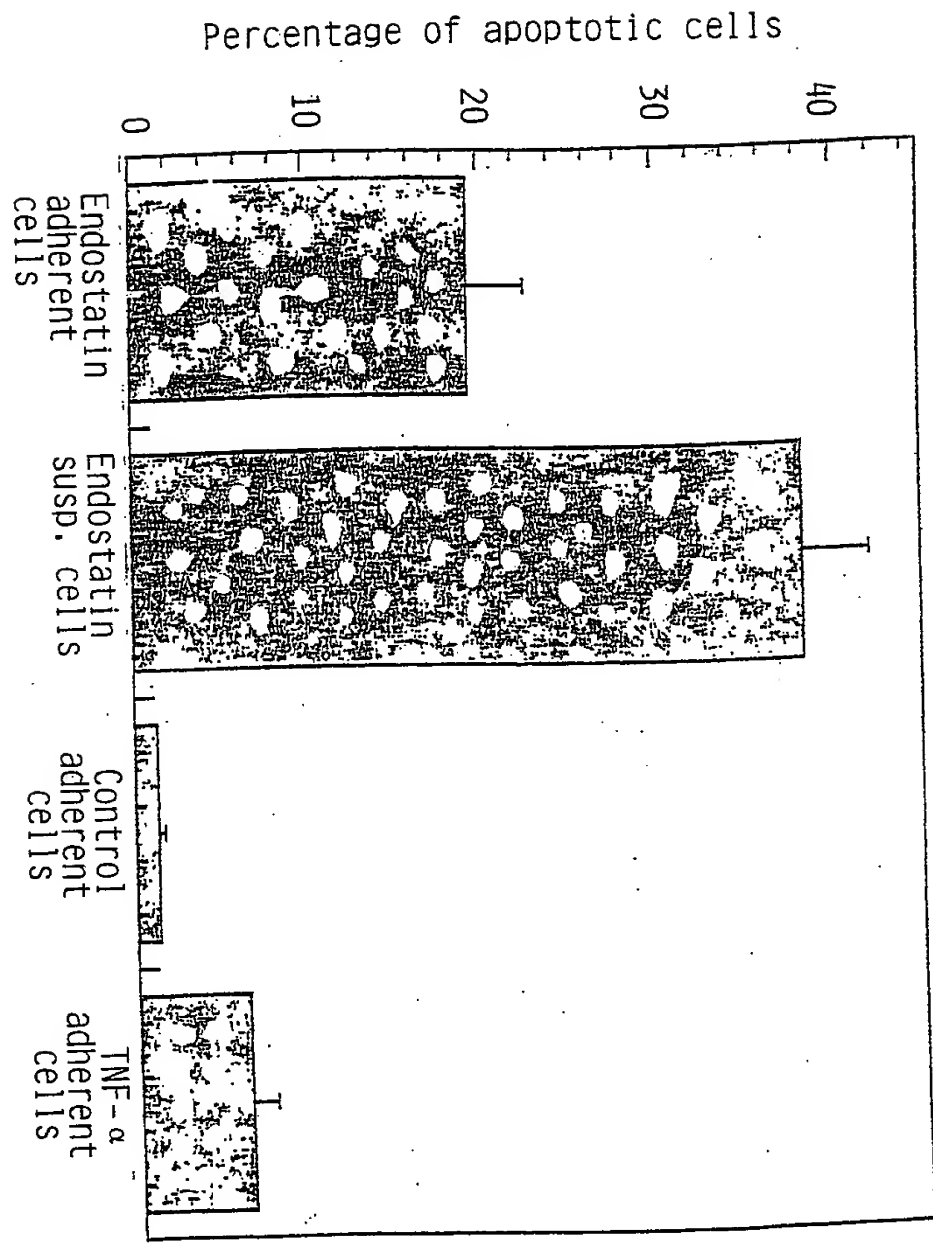


Fig. 23



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1440, 1023-011

FIG.24A

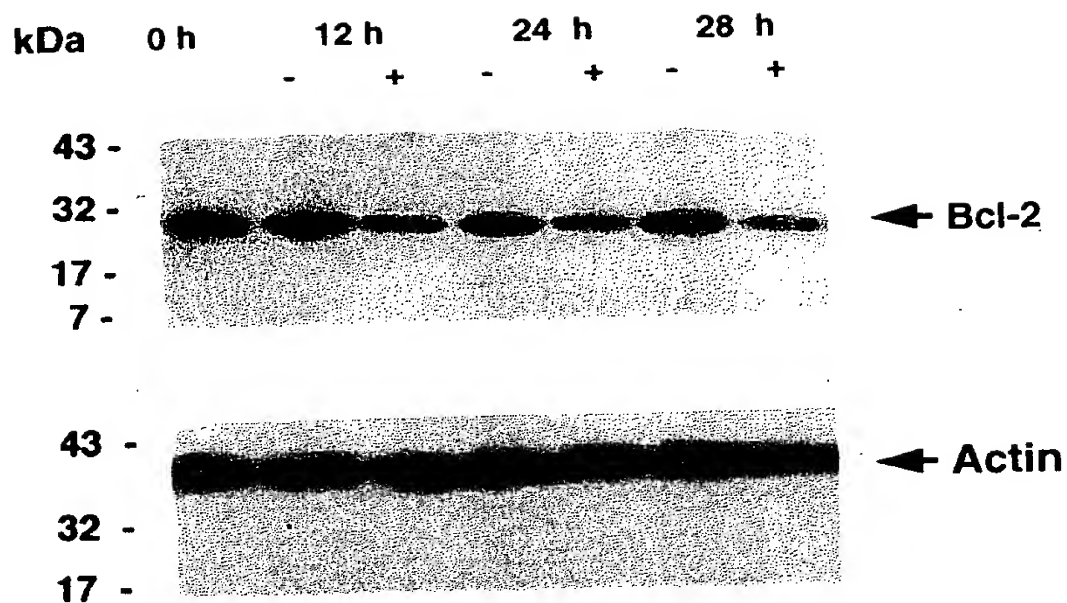
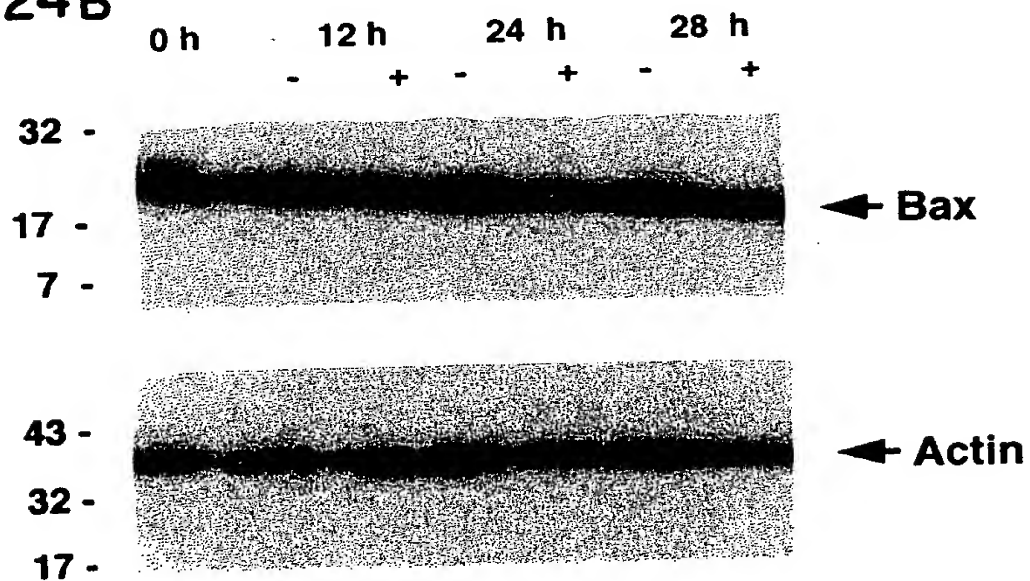


FIG.24B



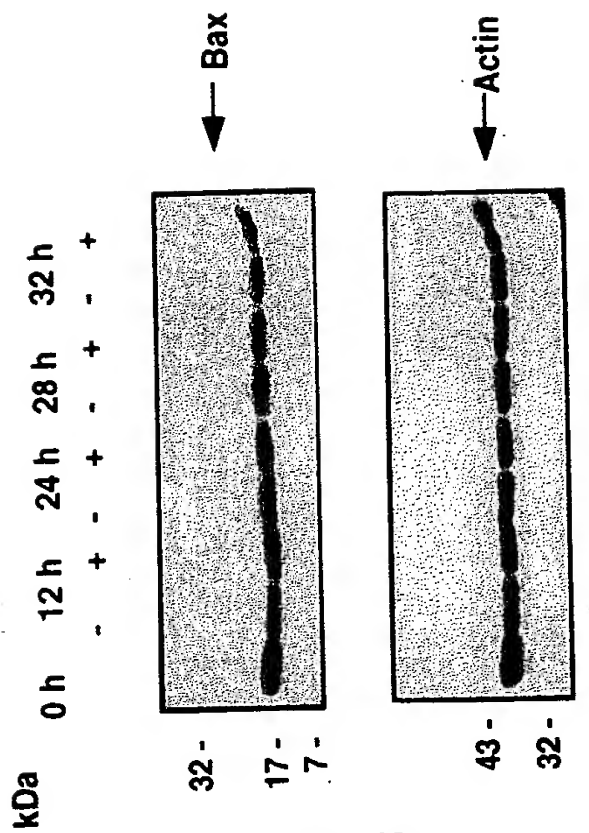


Fig. 25B

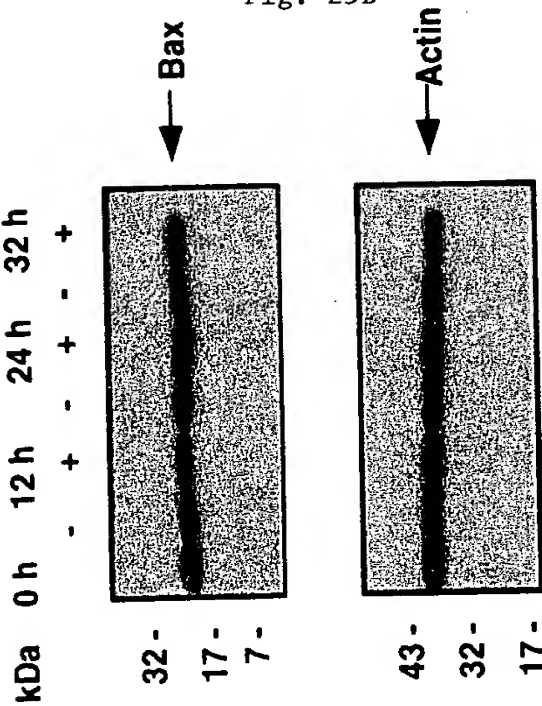


Fig. 25A

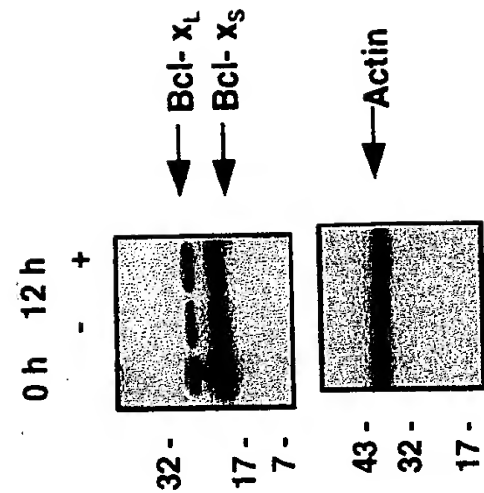


Fig. 25 D

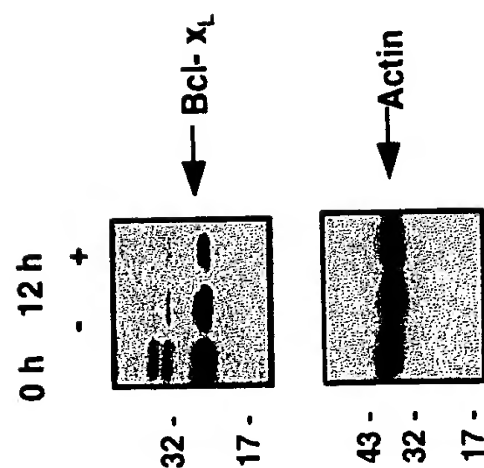


Fig. 25C

Construct Name	Primer Sequence	Cloning Sites	Vector	Protein Sequence
pET17b/ his.mendo	5'-GGC ATA TGC ATA CTC ATC AGG- ACT TT-3' (up) (SEQ ID NO:3)	NdeI & XhoI	Prokaryotic expression, pET	MGHHHHHHHHHHSSGHIDDDDKH M-mendo (SEQ ID NO:5)
	5' AAC TCG AGC TAT TTG GAG AAA- GAG GT-3' (down) (SEQ ID NO:4)			
pET28a/ mendo	5'-GGC ATA TGC ATA CTC ATC AGG- ACT TT-3' (up) (SEQ ID NO:3)	NdeI & NotI	Prokaryotic expression, pET	MGSSHHHHHHSSGLVPRGSHM- mendo (SEQ ID NO:7)
	5'-AAG CCG CCG CCT ATT TGG AGA- AAG AGG T-3' (down) (SEQ ID NO:6)			
pET28a/ EM-1	5' TTC CAT ATG CAT ACT CAT CAG- GAC TTT CAG CCA-3' (up) (SEQ ID NO:8)		Prokaryotic expression, pET	MGSSHHHHHHSSGLVPRGSHM-me ndo (SEQ ID NO:7)
	5' TTA GCG GCC GCC TAC TCA ATG- CAC AGG ACG ATG TA-3' (down) (SEQ ID NO:9)			
pET28a/ EM-2	5' TTC CAT ATG CAT ACT CAT CAG- GAC TTT CAG CCA-3' (up) (SEQ ID NO:8)		Prokaryotic expression, pET	MGSSHHHHHHSSGLVPRGSHM-me ndo (SEQ ID NO:7)
	5' TTA GCG GCC GCC TAG TTG TGG- CAG CTC GCA GCT TTC TG-3' (down) (SEQ ID NO:10)			

Fig. 26A

Construct Name	Primer Sequence	Cloning Sites	Vector	Protein Sequence
pPICZ $\alpha$ A/ mendo	5' GGG AAT TCC ATA CTC ATC AGG- ACT TT-3' (up) (SEQ ID NO:11)	<i>Eco</i> RI & <i>Not</i> I	Eukaryotic expression, yeast/pPICZ $\alpha$ A	EF-mendo
	5' AAG CGG CCG CCT ATT TGG AGA- AAG AGG T-3' (down) (SEQ ID NO:6)			
pPICZ $\alpha$ A/ His.mendo	5' AAG AAT TCC ATC ATC ATC ATC- ATC ACA GCA GC-3' (up) (SEQ ID NO:12)	<i>Eco</i> RI & <i>Not</i> I	Eukaryotic expression, yeast/pPICZ $\alpha$ A	EFMGHHHHHHHHSSGHIDDDD KHM-mendo (SEQ ID NO:13)
	5' AAG CGG CCG CCT ATT TGG AGA- AAG AGG T-3' (down) (SEQ ID NO:6)			
pPICZ $\alpha$ A/ Hendo	5' TTT GAA TTC GCC CAC AGC CAC- CGC GAC TTC CAG CCG GTG CTC- CA-3' (up) (SEQ ID NO:14)	<i>Eco</i> RI & <i>Not</i> I	Eukaryotic expression, yeast/pPICZ $\alpha$ A	EF-hendo
	5' AAA AGC GGC CGC CTA CTT GGA- GGC AGT CAT GAA GCT GTT CTC- AA-3' (down) (SEQ ID NO:15)			
pPICZ $\alpha$ A/ Restin	5' TTT TTT GAA TTC ATT TCA AGT- GCC AAT TAT GAG AAG CCT GCT CTG CAT TTG-3' (up) (SEQ ID NO:16)	<i>Eco</i> RI & <i>Not</i> I	Eukaryotic (Yeast), Pichia, pPICZ $\alpha$ A	EF-restin
	5' AAG AAT GCG GCC GCT TAC TTC- CTA GCG TCT GTC ATG AAA CTG- TTT TCG AT-3' (down) (SEQ ID NO:17)			

Fig. 26B



Construct Name	Primer Sequence	Cloning Sites	Vector	Protein Sequence
pPICZ $\alpha$ A/ His.Restin	5' AAT TCC ATC ACC ATC ACC ATC- ACG-3' (up) (SEQ ID NO:18)	<i>Eco</i> RI (oligo insertion)	Eukaryotic (Yeast), Pichia, pPICZ $\alpha$ A	EFHHHHHHH-restin (SEQ ID NO:20)
	5' AAT TCG TGA TGG TGA TGG TGA-TGG-3' (down) (SEQ ID NO:19)			
pET28a/ apomigren	5' TTC CAT ATG ATA TAC TCC TTT- GAT GGT CGA GAC ATA ATG ACA-3' (up) (SEQ ID NO:21)	<i>Nde</i> I & <i>Not</i> I	Prokaryotic, pET system	MGSSHHHHHHSSGLVPRGSHM-apo migren (SEQ ID NO:7)
	5' AAT GCG GCC GCT TAC TTC CTA- GCG TCT GTC ATG AAA CTG TTT- TCG AT-3' (down) (SEQ ID NO:22)			
pPICZ $\alpha$ A/ apomigren	5' AAG AAT TCC ATC ATC ATC ATC- ATC ACA GCA GC-3' (up) (SEQ ID NO:12)	<i>Eco</i> RI & <i>Not</i> I	Eukaryotic (Yeast), Pichia, pPICZ $\alpha$ A	EFMGSSHHHHHHSSGLVPRGSHM-apomigren (SEQ ID NO:23)
	5' AAT GCG GCC GCT TAC TTC CTA- GCG TCT GTC ATG AAA CTG TTT- TCG AT-3' (down) (SEQ ID NO:22)			

Fig. 26C